

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 11, 2005, 16:49:33 ; Search time 2179 Seconds
(without alignments)
6079.103 Million cell updates/sec

Title: US-09-824-134-1_COPY_388_735
Perfect score: 348
Sequence: 1 TTTCGAGCGGGGGCGGCGC.....GGGCGATGTCGCCGATGTCA 348

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	348	100.0	719	2	BE275002 601122536
2	348	100.0	774	2	BE275052 601122604
3	348	100.0	850	5	BU957269 AGENCOURT
4	348	100.0	931	5	BU535532 AGENCOURT
5	348	100.0	940	5	BQ672502 AGENCOURT
6	348	100.0	947	5	BU197303 AGENCOURT
7	348	100.0	965	1	AL548504 AL548504
8	348	100.0	993	1	AL527771 AL527771
9	348	100.0	1029	9	AY401682 Homo sapi
10	348	100.0	1134	1	AL544558 AL544558
11	348	100.0	1595	3	CR595812 full-leng
12	348	100.0	1595	3	CR615437 full-leng
13	348	100.0	1614	3	CR621957 full-leng
14	348	100.0	1618	3	CR591208 full-leng
15	348	100.0	1629	3	CR616586 full-leng
16	348	100.0	1634	3	CR608391 full-leng
17	348	100.0	1650	3	CR596013 full-leng
18	348	100.0	1653	3	CR593331 full-leng
19	348	100.0	1653	3	CR607000 full-leng
20	348	100.0	1663	3	CR593101 full-leng
21	348	100.0	1689	3	BC025733 Homo sapi
22	348	100.0	1691	3	CR600474 full-leng
23	348	100.0	1702	3	CR610334 full-leng
24	348	100.0	1721	3	CR599691 full-leng

25	348	100.0	1806	3	CR605817 full-leng
26	347.6	99.9	949	1	AL552532 AL552532
27	346.8	99.7	1016	1	AL527192 AL527192
28	346.8	99.7	1036	5	BX441966 BX441966
29	346.4	99.5	806	4	B1465298 B1465298
30	345.2	99.2	1061	1	AL518571 AL518571
31	344.8	99.1	614	2	AW245754 AW245754
32	344.8	99.1	937	2	BE784749 BE784749
33	344.4	99.0	870	5	BX448882 BX448882
34	343.6	98.7	1035	1	AL557131 AL557131
35	341	98.0	1099	5	BX354591 BX354591
36	337	96.8	885	4	B1193429 B1193429
37	337	96.8	887	7	CF264787 CF264787
38	337	96.8	1084	2	BE794964 BE794964
39	336.6	96.7	1023	5	BX331772 BX331772
40	336.6	96.7	1038	1	AL528496 AL528496
41	336	96.6	754	2	BE563599 BE563599
42	336	96.6	870	2	BE888978 BE888978
43	336	96.6	1015	2	BE728742 BE728742
44	335.8	96.5	1107	1	AL556073 AL556073
45	335.4	96.4	859	4	BG751059 BG751059

ALIGNMENTS

RESULT 1
BE275002 719 bp mRNA linear EST 13-JUL-2000
LOCUS 601122536F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346617 5',
DEFINITION mRNA sequence.
ACCESSION BE275002
VERSION BE275002.1 GI:9149952
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 719)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC/DCRP/DTTP
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCW136 row: h column: 10
High quality sequence stop: 717.
Location/Qualifiers
1. 719
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3346617"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

FEATURES
source

ORIGIN

Query Match 100.0%; Score 348; DB 2; Length 719;
Best Local Similarity 100.0%; Pred. No. 1.2e-83;

[illegible]

RESULT 2	774 bp	linear	EST 13-JUL-2000		
BE275052	601124604F1 NIH_MGC_20 Homo sapiens	cDNA clone IMAGE:3346608 5',			
LOCUS	mRNA sequence.				
DEFINITION	BE275052				
ACCESSION	BE275052.1	GI:9150002			
VERSION					
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabbs-remail.nih.gov Tissue Procurement: ATCC/DCTD/BTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: L12CM136 row: h column: 01 High quality sequence stop: 733.				

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FEATURES
source
1. .774
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone_image="3346608"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 20"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into EORI/XhoI sites using the following 5'
adaptor: GGACACGAG (G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

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Query Match
100.0%; Score 348; DB 2; Length 774;

[illegible]

RESULT 3	
BUS957269	
LOCUS	850 bp mRNA linear EST 21-OCT-2002
DEFINITION	AGENCOURT 10622000 NIH_MGC_107 Homo sapiens cDNA clone IMAGE:6731271 5', mRNA_sequence.
ACCESSION	BUS957269
VERSION	BUS957269.1 GI:24186841
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 850) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC CDNA library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCW3057 row: g column: 14 High quality sequence stop: 650.
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

FEATURES source

ORIGIN

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Note: this is a NIH_MGC Library."

ORIGIN
Query Match      100.0%; Score 348; DB 5; Length 931;
Best Local Similarity 100.0%; Pred. NO. 1.3e-83;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 TTGAGCGGGGGCGGGCGGGCGGGCGGGCGGGCGGGGAAGAAGACCTGTGTGCGACGATTT 60
    |||
Db   92 TTGAGCGGGGGCGGGCGGGCGGGCGGGCGGGCGGGGAAGAAGACCTGTGTGCGACGATTT 151
    |||

Qy   61 AACGTCAATGTGTAATGTGTGGGAAAGATTGGAGAGGCTGGGTCGTGACGTCAAAGTC 120
    |||
Db   152 AACGTCAATGTGTAATGTGTGGGAAAGATTGGAGAGGCTGGGTCGTGACGTCAAAGTC 211
    |||

Qy   121 TCAGACACCAGATCGACAGCATCGAGGACAGATACCCCGCAACCTTGACAGAGCGTGTG 180
    |||
Db   212 TCAGACACCAGATCGACAGCATCGAGGACAGATACCCCGCAACCTTGACAGAGCGTGTG 271
    |||

Qy   181 CGGGAGTCACTGAGAAATCTGGAAGAACACAGAGAAAGGAGAACGCCAAGTGCGCCACCTG 240
    |||
Db   272 CGGGAGTCACTGAGNAITCTGGNAGAACACAGAGAAAGGAGAACGCCAAGTGCGCCACCTG 331
    |||

Qy   241 GTGGGGGCTCTCAGGTCTCTGCAGATGAACCTGGTGGCTGACTCTGGTAACAAGAGTTCCAG 300
    |||
Db   332 GTGGGGGCTCTCAGGTCTCTGCCAGATGAACCTGGTGGCTGACCTTGGTACAAAGAGTTCCAG 391
    |||

Qy   301 CAGGCCCGTGACTCCAGAACAGAGAGTGGGGCCATGTCCCCCGATGTCA 348
    |||
Db   392 CAGGCCCGTGACTCCAGAACAGAGAGTGGGGCCATGTCCCCCGATGTCA 439
    |||

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RESULT 5	
BQ672502	940 bp mRNA linear EST 15-JUL-2000
LOCUS	AGNCOUNT 8349344 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6276351
DEFINITION	5', mRNA sequence.
ACCESSION	BQ672502
VERSION	BQ672502.1 GI:21783336
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1. (bases 1 to 940)
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: L1CM2460 row: p column: 15 High quality sequence stop: 488.

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FEATURES
source
high quality sequence (top: 100.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6276350"
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NTH MGC_102"
/note="Organ: salivary gland; Vector: pOTB7; Site 1: XhoI
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin

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[illegible]

RESULT 4	BU535532	931 bp	mRNA	linear	EST 13-SEP-2002
OCUS	AGENCOURT 10217577	NIH MGC 107	Homo sapiens	CDNA clone	
DEFINITION	IMAGE:6563185	5', mRNA	sequence.		
CCESSION	BU535532				
ERSION	BU535532.1	GI:22845973			
EWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
	1 (bases 1 to 931)				
REFERENCE	NIH-MGC http://(mgc.nci.nih.gov/.				
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)				
TITLE	Unpublished (1999)				
JOURNAL	Contact: Robert Strausberg, Ph.D.				
COMMENT	Email: cgabs@mail.nih.gov				
	Tissue procurement: ARCC				
	CDNA Library Preparation: Rubin Laboratory				
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)				
	DNA Sequencing by: Agencourt Bioscience Corporation				
	Clone distribution: MGC clone distribution information can be				
	found through the I.M.A.G.E. Consortium/LLNL at:				
	http://image.llnl.gov				
	Plate: LLCW2740	row: 01			
	High quality	sequence	stop: 506.		

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FEATURES
    source
        1. .931
            Location/Qualifiers
                organism="Homo sapiens"
                mol_type="mRNA"
                db_xref="taxon:9606"
                clone="IMAGE:6563185"
                tissue_type="adenocarcinoma, cell line"
                lab_host="DH10B (phage-resistant)"
                clone_lib="NIH_MGC_107"
                notes="Organ: breast; Vector: pOTB7; Site_1: EcoRI;
                    Site_2: XhoI; cDNA made by oligo-dr priming.
                    Directionally cloned into EcoRI/XhoI sites using the
                    following 5' adaptor: GGCACGAG(G). Library constructed by
                    Ling Hong in the laboratory of Gerald M. Rubin (University
                    of California, Berkeley) using zap-cDNA synthesis kit
                    (Stratagene) and Superscript II RT (Life Technologies)."

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328	TTGAGGCGGGCGGCGCGCGCGCTGGGGAAGAGACCTGTGTGTCAGCATTT	387
61	AACGTCATATGTGATAATGTGGGAAAAGATTGGAGAAAGCTGGCTCGTCAGCTCAAGTC	120
388	AACGTCATATGTGATAATGTGGGAAAAGATTGGAGAAAGCTGGCTCGTCAGCTCAAGTC	447
121	TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCGCAACCTGACAGAGCGGTGTG	180
448	TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCGCAACCTGACAGAGCGGTGTG	507
181	CGGGAGTCATCTGAGAAATCTGGAAAGAACACAGAGAGGAGAACCCACAGTGGGCCACCTG	240
508	CGGGAGTCATCTGAGAAATCTGGAAAGAACACAGAGAGGAGAACCCACAGTGGGCCACCTG	567
241	GTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAAGAGTTTCAG	300
568	GTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAAGAGTTTCAG	627
301	CAGGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA	348
628	CAGGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA	675

RESULT 13	
CR621957	
LOCUS	1614 bp mRNA linear HTC 21-JUL-2004
DEFINITION	full-length cDNA clone CSODI067yD16 of Placenta Cot 25-normalized of Homo sapiens (human).
ACCESSION	CR621957
VERSION	CR621957.1 GI:50502764
KEYWORDS	HTC; CNSLT_CDNA.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 1614)
AUTHORS	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Paraday Avenue
REFERENCE	2 (bases 1 to 1614)

TITLE Direct Submission
SUBMITTED 120-JUL-2004 Genoscope - Centre National de Sequencage
JOURNAL Submitted (20-JUL-2004) Genoscope - FRANCE (E-mail : seque@genoscope.cns.fr)
 Bp 191 91006 EVRY cedex - FRANCE
 - Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primers
 into enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
FEATURES Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="CS0D1067YD16"
 /tissue_type="Placenta Cot 25-normalized"
 /plasmid="pCMVSPORT 6"

FEATURES
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 Location/Qualifiers
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 /mol_type="mRNA"
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 Query Match 100.0%; Score 348; DB 3; Length 1614;
 Best Local Similarity 100.0%; Pred. NO. 1.4e-83;
 Watches 348. Conservative 0; Mismatches 0; Gaps 0

[illegible]

Db 556 CGGGAGTCACTGAGAAATCTGAAGAAACACAGAGAGAGAGAGACGCAACAGTGGCCCCACCTG 615
Qy 241 GTGGGGGCTCTCAGGTCTCTGCCAGATGAACCTGGTGGCTGACCTGGTACAGAGGTTTCAG 300
Db 616 GTGGGGGCTCTCAGGTCTCTGCCAGATGAACCTGGTGGCTGACCTGGTACAGAGGTTTCAG 675
Qy 301 CAGGGCCCGTGACCTCCAGAAACAGGAGTGGGGGCCATGTCCCCGATGTCA 348
Db 676 CAGGGCCCGTGACCTCCAGAAACAGGAGTGGGGGCCATGTCCCCGATGTCA 723

Search completed: February 11, 2005, 20:33:32
Job time : 2185 secs

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